Phage therapy, a practice widespread in Eastern Europe, has untapped potential in the combat against antibiotic-resistant bacterial infections. However, technology transfer to Western medicine is proving challenging. Bioinformatics analysis could help to facilitate this endeavor. In the present study, the Intesti phage cocktail, a key commercial product of the Eliava Institute, Georgia, has been tested on a selection of bacterial strains, sequenced as a metagenomic sample, de novo assembled and analyzed by bioinformatics methods. Furthermore, eight bacterial host strains were infected with the cocktail and the resulting lysates sequenced and compared to the unamplified cocktail. The analysis identified 23 major phage clusters in different abundances in the cocktail, among those clusters related to the ICTV genera T4likevirus, T5likevirus, T7likevirus, Chilikevirus and Twortlikevirus, as well as a cluster that was quite distant to the database sequences and a novel Proteus phage cluster. Examination of the depth of coverage showed the clusters to have different abundances within the cocktail. The cocktail was found to be composed primarily of Myoviridae (35%) and Siphoviridae (32%), with Podoviridae being a minority (15%). No undesirable genes were found.

General information
State: Published
Organisations: Department of Systems Biology, Center for Biological Sequence Analysis, National Food Institute, Research group for Genomic Epidemiology, Department of Microbiology, Technical University of Denmark, Eliava Institute of Bacteriophages, Microbiology and Virology, Eliava Biopreparations LTD, The Evergreen State College
Number of pages: 20
Pages: 6570-6589
Publication date: 2015
Peer-reviewed: Yes

Publication information
Journal: Viruses
Volume: 7
Issue number: 12
ISSN (Print): 1999-4915
Ratings:
Web of Science (2019): Indexed yes
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 3.88 SJR 1.805 SNIP 1.13
Web of Science (2017): Impact factor 3.761
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 3.6 SJR 1.747 SNIP 1.02
Web of Science (2016): Impact factor 3.465
Web of Science (2016): Indexed yes
Scopus rating (2015): CiteScore 3.74 SJR 1.832 SNIP 1.034
Web of Science (2015): Impact factor 3.042
Web of Science (2015): Indexed yes
Scopus rating (2014): CiteScore 3.8 SJR 1.906 SNIP 1.098
Web of Science (2014): Impact factor 3.353
Scopus rating (2013): CiteScore 3.41 SJR 1.642 SNIP 0.979
Web of Science (2013): Impact factor 3.279
Scopus rating (2012): CiteScore 2.67 SJR 1.152 SNIP 0.686
Web of Science (2012): Impact factor 2.509
Scopus rating (2011): CiteScore 1.63 SJR 0.72 SNIP 0.439
Web of Science (2011): Impact factor 1.5
Scopus rating (2010): SJR 0.446 SNIP 0.21
Web of Science (2010): Impact factor 1
Original language: English
Keywords: Eliava Intestiphage, metagenomics, phage therapy, whole genome sequence analysis
Electronic versions:
viruses_07_02958.pdf
DOIs:
10.3390/v7122958